

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 7, 2005, 12:16:15 ; Search time 12 seconds  
(without alignments)  
233.150 Million cell updates/sec

Title: US-09-285-531A-2

Perfect score: 2802

Sequence: 1 MAPVAVMAALAVGLELWAAA.....PSTSFLLPMGPSPARGSTG 501

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.New.\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pap.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pap.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pap.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pap.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pap.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pap.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pap.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1421.5	50.7	461	7	US-11-132-285-6
2	1421.5	50.7	461	7	US-11-182-946-4
3	1302	46.5	235	7	US-11-126-126-16
4	381	13.6	349	7	US-11-182-946-13
5	373	13.3	355	7	US-11-182-946-14
6	371	13.2	350	7	US-11-132-285-41
7	347.5	12.4	595	7	US-11-182-946-9
8	313.5	11.2	415	7	US-11-182-946-6
9	302.5	10.8	277	7	US-11-182-946-10
10	301.5	10.8	359	7	US-11-105-172-2
11	301.5	10.8	391	7	US-11-105-172-4
12	281.5	10.0	909	7	US-11-076-187-4
13	241	8.6	211	7	US-11-132-839-12
14	239	8.5	246	7	US-11-132-839-8
15	238	8.5	195	7	US-11-132-839-11
16	238	8.5	203	7	US-11-132-839-10
17	216	7.7	669	7	US-11-076-187-3
18	215.5	7.7	833	7	US-11-076-187-5
19	212.5	7.6	160	7	US-11-132-839-7
20	208	7.4	277	7	US-11-132-285-3
21	208	7.4	277	7	US-11-182-946-12
22	193	6.9	3717	6	US-10-821-234-1076
23	189.5	6.8	685	6	US-10-131-826A-88
24	189.5	6.8	685	7	US-11-078-735-19
25	189	6.7	427	7	US-11-182-946-5

26	185	6.6	255	7	US-11-182-946-11	Sequence 11, Appli
27	180.5	6.4	455	7	US-11-182-946-3	Sequence 3, Appli
28	177	6.3	4419	6	US-10-821-234-1155	Sequence 1155, Ap
29	175	6.2	5179	7	US-11-108-172-1068	Sequence 1068, Ap
30	163.5	5.8	575	6	US-10-980-388-46	Sequence 46, Appl
31	162.5	5.8	259	6	US-10-131-826A-300	Sequence 300, Appl
32	162.5	5.8	259	7	US-11-182-946-2	Sequence 2, Appli
33	161	5.7	156	7	US-11-132-839-9	Sequence 9, Appli
34	161	5.7	161	7	US-11-126-126-2	Sequence 2, Appli
35	153.5	5.5	468	7	US-11-076-187-2	Sequence 2, Appli
36	151	5.4	334	6	US-10-514-057-6	Sequence 6, Appli
37	147.5	5.3	544	6	US-10-980-388-40	Sequence 40, Appl
38	147.5	5.3	1076	6	US-10-131-826A-219	Sequence 219, Appl
39	144.5	5.2	106	7	US-11-126-126-4	Sequence 4, Appli
40	144.5	5.2	106	7	US-11-126-126-8	Sequence 8, Appli
41	144.5	5.2	109	7	US-11-182-946-6	Sequence 6, Appli
42	141	5.0	335	7	US-11-182-946-7	Sequence 7, Appli
43	140	5.0	101	7	US-11-126-126-12	Sequence 12, Appli
44	140	5.0	1028	7	US-11-067-121-7	Sequence 7, Appli
45	140	5.0	1036	6	US-10-131-826A-142	Sequence 142, App

#### ALIGNMENTS

RESULT 1  
US-11-132-285-6  
; Sequence 6, Application US/11132285  
; Publication No. US20050244876A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR13 and TR14  
; FILE REFERENCE: PFS11PI  
; CURRENT APPLICATION NUMBER: US/11/132,285  
; CURRENT FILING DATE: 2005-05-19  
; PRIOR APPLICATION NUMBER: US/10/046,433  
; PRIOR FILING DATE: 2002-01-16  
; PRIOR APPLICATION NUMBER: 60/261,960  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 09/618,570  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/144,087  
; PRIOR FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: 60/149,450  
; PRIOR FILING DATE: 1999-07-18  
; PRIOR APPLICATION NUMBER: 60/149,712  
; PRIOR FILING DATE: 1999-08-20  
; PRIOR APPLICATION NUMBER: 60/153,089  
; PRIOR FILING DATE: 1999-09-10  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 6

; LENGTH: 461

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-132-285-6

Query Match 50.7%; Score 1421.5; DB 7; Length 461;  
Best Local Similarity 58.4%; Pred No. 1.7e-85;  
Matches 301; Conservative 30; Mismatches 97; Indels 87; Gaps 12;

QY	1	MAPVAVMAALAVGLELWAAAALPAQVAFTPYAPFGSTCRLEYYDQTAQMCCSKCSPG	60
Db	1	MAPVAVMAALAVGLELWAAAALPAQVAFTPYAPFGSTCRLEYYDQTAQMCCSKCSPG	60
QY	61	QKAVFCTKTDVCDSCEDSTYTLQMNWPECLSCGRCSDDQVETQACTREQNRCTC	120
Db	61	QKAVFCTKTDVCDSCEDSTYTLQMNWPECLSCGRCSDDQVETQACTREQNRCTC	120
QY	121	RPGWYCALSKOEGCRCLCAPLRKCRPGFGVARPGTETSDVCKPCAPGTFSTNTSDICR	180
Db	121	RPGWYCALSKOEGCRCLCAPLRKCRPGFGVARPGTETSDVCKPCAPGTFSTNTSDICR	180

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OM protein - protein search, using sw model

Run on: December 7, 2005, 12:16:00 ; Search time 165 Seconds

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1268.682 Million cell updates/sec

Title: US-09-285-531A-2

Perfect score: 2802

Sequence: 1 MAPVAVMAALAVGLELWAAA.....PSTSFLLPMGSPPAEGSTG 501

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA\_Main:  
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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pcp.\*  
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4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pcp.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pcp.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2674.5	95.4	720	4	US-10-363-427-8
2	2332	83.2	659	4	US-10-363-427-12
3	1429.5	51.0	566	5	US-10-677-877A-10
4	1427.5	50.9	461	3	US-09-800-909-2
5	1427.5	50.9	461	3	US-09-758-124-2
6	1427.5	50.9	461	3	US-09-800-908-3
7	1427.5	50.9	461	3	US-09-902-176A-50
8	1427.5	50.9	461	3	US-09-902-176A-52
9	1427.5	50.9	461	4	US-10-164-592-3
10	1427.5	50.9	461	4	US-10-252-408-2
11	1427.5	50.9	461	4	US-10-420-785-2
12	1427.5	50.9	461	4	US-10-423-927-2
13	1427.5	50.9	461	4	US-10-411-037-32
14	1427.5	50.9	461	4	US-10-411-026-32
15	1427.5	50.9	461	4	US-10-410-962-32
16	1427.5	50.9	461	4	US-10-411-049-32
17	1427.5	50.9	461	4	US-10-410-930-32
18	1427.5	50.9	461	4	US-10-410-997-32
19	1427.5	50.9	461	4	US-10-411-012-32
20	1427.5	50.9	461	4	US-10-287-994-32
21	1427.5	50.9	461	4	US-10-410-913-32
22	1427.5	50.9	461	4	US-10-632-929-3
23	1427.5	50.9	461	4	US-10-748-112-9
24	1427.5	50.9	461	5	US-10-370-715B-112
25	1427.5	50.9	461	5	US-10-410-980-32
26	1427.5	50.9	461	5	US-10-901-735-1
27	1427.5	50.9	461	5	US-10-775-180-152

Sequence 155, App  
Sequence 32, Appl  
Sequence 32, Appl  
Sequence 462, App  
Sequence 467, App  
Sequence 112, App  
Sequence 12, Appl  
Sequence 4, Appl  
Sequence 17, Appl  
Sequence 17, Appl  
Sequence 17, Appl  
Sequence 6, Appl  
Sequence 54, Appl  
Sequence 6, Appl  
Sequence 17, Appl  
Sequence 4, Appl  
Sequence 6, Appl  
Sequence 17, Appl  
Sequence 6, Appl  
Sequence 17, Appl  
Sequence 17, Appl

#### ALIGNMENTS

RESULT 1  
US-10-363-427-8  
; Sequence 8, Application US/10363427  
; Publication No. US20030195338A1  
; GENERAL INFORMATION:  
; APPLICANT: MeDexGen Inc.  
; APPLICANT: CHUNG, Yong Hoon  
; APPLICANT: HAN, Ji Woong  
; APPLICANT: LEE, Hye Ja  
; APPLICANT: CHOI, Eun Yong  
; APPLICANT: KIM, Jin Mi  
; APPLICANT: YIM, Soo Bin  
; TITLE OF INVENTION: Concatametric Immunoadhesion  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/363,427  
; CURRENT FILING DATE: 2003-02-28  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: KopatentIn 1.71  
; SEQ ID NO 8  
; LENGTH: 720  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-363-427-8

Query Match 95.4%; Score 2674.5; DB 4; Length 720;  
Best Local Similarity 96.0%; Pred. No. 9.9e-149;  
Matches 481; Conservative 1; Mismatches 4; Indels 15; Gaps 1;  
Qy 1 MAPVAVMAALAVGLELWAAAHALPAQVAFTPYAPPGSTCKRLREYDYDTAQMCCSKCSPG 60  
Db 1 MAPVAVMAALAVGLELWAAAHALPAQVAFTPYAPPGSTCKRLREYDYDTAQMCCSKCSPG 60  
Qy 61 QHAKVCTKTSDTVCDSCESTYTLNWNVPECLSCGRCSSDDQVETQACTREQNRITC 120  
Db 61 QHAKVCTKTSDTVCDSCESTYTLNWNVPECLSCGRCSSDDQVETQACTREQNRITC 120  
Qy 121 RQGWYCALSKOEGRCLCAPLRCRPGFVARPGTETSDVVKPCAPGTFSTSTDI 180  
Db 121 RQGWYCALSKOEGRCLCAPLRCRPGFVARPGTETSDVVKPCAPGTFSTSTDI 180  
Qy 181 PHQICNVVAIPGNASMDAVCTSTPSTRMAPAGVHLPPQVSTRQHTQPTPEPSTAPSTS 240  
Db 181 PHQICNVVAIPGNASMDAVCTSTPSTRMAPAGVHLPPQVSTRQHTQPTPEPSTAPSTS 240  
Qy 241 FLLPMGSPPARGGGSGGGSGGGSDPAQVAFTPYAPPGSTCKRLREYDYDTAQMCCS 300  
Db 241 FLLPMGSPPARGGGSGGGSGGGSDPAQVAFTPYAPPGSTCKRLREYDYDTAQMCCS 285  
Qy 301 KCSPGOHAKVCTKTSDTVCDSCESTYTLNWNVPECLSCGRCSSDDQVETQACTREQNRITC 360  
Db 301 KCSPGOHAKVCTKTSDTVCDSCESTYTLNWNVPECLSCGRCSSDDQVETQACTREQNRITC 360

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OM protein - protein search, using sw model

Run on: December 7, 2005, 12:10:29 ; Search time 26 Seconds  
(without alignments)  
1593.097 Million cell updates/sec

Title: US-09-285-531A-2  
Perfect score: 2802  
Sequence: 1 MAPVAVMAALVGLLEWAAA.....PSTFLLPMGSPPPAGSTG 501

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA\*  
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2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/H COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1427.5	50.9	461	1	US-08-385-229-2
2	1427.5	50.9	461	1	US-08-650-000-2
3	1427.5	50.9	461	2	US-08-477-347-3
4	1427.5	50.9	461	2	US-08-476-862-2
5	1427.5	50.9	461	2	US-08-406-824A-2
6	1427.5	50.9	461	2	US-09-800-909-2
7	1427.5	50.9	461	2	US-09-758-124-2
8	1427.5	50.9	461	2	US-09-800-908-3
9	1427.5	50.9	461	2	US-09-949-016-6019
10	1427.5	50.9	461	6	5395760-2
11	1427.5	50.9	491	2	US-09-949-016-7840
12	1421.5	50.7	461	2	US-09-042-785A-7
13	1421.5	50.7	461	2	US-09-006-333A-4
14	1421.5	50.7	461	2	US-09-573-986-4
15	1421.5	50.7	461	2	US-09-896-096A-17
16	1421.5	50.7	461	2	US-10-046-433-6
17	1409	50.3	257	2	US-09-579-845-10
18	1409	50.3	518	1	US-08-385-229-4
19	1409	50.3	518	2	US-09-573-845-1
20	1409	50.3	518	2	US-09-579-845-3
21	1402	50.0	486	1	US-08-243-010-1
22	1308.5	46.7	439	2	US-10-360-101-226
23	1308	46.7	235	2	US-09-580-235-8
24	1308	46.7	235	2	US-09-580-181-8
25	1308	46.7	235	2	US-09-102-530-8
26	1305	46.6	235	2	US-09-580-235-2
27	1305	46.6	235	2	US-09-580-235-4

28	1305	46.6	235	2	US-09-580-181-2	Sequence 2, Appli
29	1305	46.6	235	2	US-09-580-181-4	Sequence 4, Appli
30	1305	46.6	235	2	US-09-102-530-2	Sequence 2, Appli
31	1305	46.6	235	2	US-09-102-530-4	Sequence 4, Appli
32	1302	46.5	235	2	US-09-326-394-4	Sequence 4, Appli
33	1302	46.5	235	2	US-09-580-235-6	Sequence 6, Appli
34	1302	46.5	235	2	US-09-580-181-6	Sequence 6, Appli
35	1302	46.5	235	2	US-09-102-530-6	Sequence 6, Appli
36	1263	45.1	227	2	US-08-974-022-48	Sequence 48, Appl
37	1263	45.1	227	2	US-08-795-445A-48	Sequence 48, Appl
38	1263	45.1	227	2	US-08-795-447A-48	Sequence 48, Appl
39	1263	45.1	227	2	US-08-974-186-48	Sequence 48, Appl
40	1263	45.1	227	2	US-08-795-446B-48	Sequence 48, Appl
41	1263	45.1	227	2	US-08-706-945D-134	Sequence 134, App
42	1263	45.1	227	2	US-08-577-788C-48	Sequence 48, Appl
43	1068	38.1	189	2	US-09-422-680A-25	Sequence 25, Appl
44	935	33.4	163	2	US-09-523-323-54	Sequence 54, Appl
45	931	33.2	163	1	US-08-219-237B-5	Sequence 5, Appli

## ALIGNMENTS

## RESULT 1

US-08-385-229-2  
; Sequence 2, Application US/08385229  
; Patent No. 5605690  
; GENERAL INFORMATION:

; APPLICANT: Jacobs, Cindy A.

; APPLICANT: Smith, Craig A.

; TITLE OF INVENTION: Method of Treating TNF-Dependent

; TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: Washington

; COUNTRY: U.S.A.

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/385,229

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/946,236

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Wight, Christopher L.

; REGISTRATION NUMBER: 31,680

; REFERENCE/DOCKET NUMBER: 2503

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 587-0430

; TELEFAX: (206) 587-0606

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 461 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-385-229-2

Query Match 50.9%; Score 1427.5; DB 1; Length 461;

Best Local Similarity 58.6%; Pred. No. 33e-94;

Matches 302; Conservative 30; Mismatches 96; Indels 87; Gaps 12;

Qy 1 MAPVAVMAALVGLLEWAAHALPAQVAFYAPPGSTCLREYDDTAQMCCSKSPG 60

|||||